



PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/089,485

DATE: 04/17/2002
TIME: 12:16:40

Input Set : A:\62489.txt
Output Set: N:\CRF3\04172002\J089485.raw

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3 <110> APPLICANT: Hanada and Yang
5 <120> TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-5 (FGF-5) IS A TUMOR
6 ASSOCIATED T-CELL ANTIGEN
8 <130> FILE REFERENCE: 55911
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/089,485
C--> 11 <141> CURRENT FILING DATE: 2002-03-27
    13 <150> PRIOR APPLICATION NUMBER: PCT/US00/26689
    14 <151> PRIOR FILING DATE: 2000-09-29
    16 <150> PRIOR APPLICATION NUMBER: 60/157,103
    17 <151> PRIOR FILING DATE: 1999-10-02
    19 <160> NUMBER OF SEQ ID NOS: 25
    21 <170> SOFTWARE: PatentIn Ver. 2.1
    23 <210> SEQ ID NO: 1
    24 <211> LENGTH: 143
    25 <212> TYPE: DNA
    26 <213> ORGANISM: Homo sapiens
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    30 <222> LOCATION: (27)..(140)
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        Met Ser Thr Arg Cys Gly Glu Ala Gly
    34             1           5
    35
    37 aqa gcc aga ggc acg cag ccg cac agg ggc tac aga gcc cag aat caa 101
    38 Arg Ala Arg Gly Thr Gln Pro His Arg Gly Tyr Arg Ala Gln Asp
    39   10          15          20
    41 ccc tac aag atg cac tta gga ccc ccg cgg ctg gaa gaa tga      143
    42 Pro Tyr Lys Met His Leu Gly Pro Pro Arg Leu Glu Glu
    43       30          35
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    47 <211> LENGTH: 38
    48 <212> TYPE: PRT
    49 <213> ORGANISM: Homo sapiens
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    55 His Arg Gly Tyr Arg Ala Gln Asn Gln Pro Tyr Lys Met His Leu Gly
    56       20          25          30
    58 Pro Pro Arg Leu Glu Glu
    59             35
    63 <210> SEQ ID NO: 3
    64 <211> LENGTH: 1123
    65 <212> TYPE: DNA

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66 <213> ORGANISM: Homo sapiens
 68 <220> FEATURE:
 69 <221> NAME/KEY: CDS
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 75 gaggcacgca gcccacagg ggctacagag cccagaatca gcctacaag atgcacttag 120
 77 gaccccccgcg gctgaaaga atg agc ttg tcc ttc ctc ctc ctc ttc ttc 172
 78 Met Ser Leu Ser Phe Leu Leu Leu Phe Phe
 79 1 5 10
 81 agc cac ctg atc ctc agc gcc tgg gct cac ggg gag aag cgt ctc gcc 220
 82 Ser His Leu Ile Leu Ser Ala Trp Ala His Gly Glu Lys Arg Leu Ala
 83 15 20 25
 85 ccc aaa ggg caa ccc gga ccc gct gcc act gat agg aac cct ata ggc 268
 86 Pro Lys Gly Gln Pro Gly Pro Ala Ala Thr Asp Arg Asn Pro Ile Gly
 87 30 35 40
 89 tcc agc agc aga cag agc agt agc gct atg tct tcc tct tct gcc 316
 90 Ser Ser Ser Arg Gln Ser Ser Ser Ala Met Ser Ser Ser Ala
 91 45 50 55
 93 tcc tcc tcc ccc gca gct tct ctg ggc agc caa gga agt ggc ttg gag 364
 94 Ser Ser Ser Pro Ala Ala Ser Leu Gly Ser Gln Gly Ser Gly Leu Glu
 95 60 65 70 75
 97 cag agc agt ttc cag tgg agc ccc tcg ggg cgc cg acc ggc agc ctc 412
 98 Gln Ser Ser Phe Gln Trp Ser Pro Ser Gly Arg Arg Thr Gly Ser Leu
 99 80 85 90
 101 tac tgc aga gtg ggc atc ggt ttc cat ctg cag atc tac ccg gat ggc 460
 102 Tyr Cys Arg Val Gly Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly
 103 95 100 105
 105 aaa gtc aat gga tcc cac gaa gcc aat atg tta agt gtt ttg gaa ata 508
 106 Lys Val Asn Gly Ser His Glu Ala Asn Met Leu Ser Val Leu Glu Ile
 107 110 115 120
 109 ttt gct gtg tct cag ggg att gta gga ata cga gga gtt ttc agc aac 556
 110 Phe Ala Val Ser Gln Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn
 111 125 130 135
 113 aaa ttt tta gcg atg tca aaa aaa gga aaa ctc cat gca agt gcc aag 604
 114 Lys Phe Leu Ala Met Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys
 115 140 145 150 155
 117 ttc aca gat gac tgc aag ttc agg gag cgt ttt caa gaa aat agc tat 652
 118 Phe Thr Asp Asp Cys Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr
 119 160 165 170
 121 aat acc tat gcc tca gca ata cat aga act gaa aaa aca ggg cgg gag 700
 122 Asn Thr Tyr Ala Ser Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu
 123 175 180 185
 125 tgg tat gtt gcc ctg aat aaa aga gga aaa gcc aaa cga ggg tgc agc 748
 126 Trp Tyr Val Ala Leu Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser
 127 190 195 200
 129 ccc cgg gtt aaa ccc cag cat atc tct acc cat ttt ctt cca aga ttc 796
 130 Pro Arg Val Lys Pro Gln His Ile Ser Thr His Phe Leu Pro Arg Phe
 131 205 210 215

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133	aag cag tcg qag cag cca gaa ctt tct ttc acg gtt act gtt cct gaa	844
134	Lys Gln Ser Glu Gln Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu	
135	220 225 230 235	
137	aag aaa aat cca cct agc cct atc aag tca aag att ccc ctt tct gca	892
138	Lys Lys Asn Pro Pro Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala	
139	240 245 250	
141	cct cgg aaa aat acc aac tca gtg aaa tac aga ctc aag ttt cgc ttt	940
142	Pro Arg Lys Asn Thr Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe	
143	255 260 265	
145	qqa taa tattaatctt ggccttgtga gaaaccattc tttccctca ggagtttcta	996
146	Gly	
148	taggtgtctt cagagttctg aagaaaaatt actggacaca gcttcagcta tacttacact	1056
150	gtattgaagt cacgtcattt gtttcagtgt gactgaaaca aaatgtttt tgataggaag	1116
152	gaaactg	1123
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157	<212> TYPE: PRT	
158	<213> ORGANISM: Homo sapiens	
160	<400> SEQUENCE: 4	
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163	Ser Ala Trp Ala His Gly Glu Lys Arg Leu Ala Pro Lys Gly Gln Pro	
164	20 25 30	
165	Gly Pro Ala Ala Thr Asp Arg Asn Pro Ile Gly Ser Ser Ser Arg Gln	
166	35 40 45	
167	Ser Ser Ser Ala Met Ser Ser Ser Ala Ser Ser Ser Pro Ala	
168	50 55 60	
169	Ala Ser Leu Gly Ser Gln Gly Ser Gly Leu Glu Gln Ser Ser Phe Gln	
170	65 70 75 80	
171	Trp Ser Pro Ser Gly Arg Arg Thr Gly Ser Leu Tyr Cys Arg Val Gly	
172	85 90 95	
173	Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys Val Asn Gly Ser	
174	100 105 110	
175	His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe Ala Val Ser Gln	
176	115 120 125	
177	Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys Phe Leu Ala Met	
178	130 135 140	
179	Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe Thr Asp Asp Cys	
180	145 150 155 160	
181	Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn Thr Tyr Ala Ser	
182	165 170 175	
183	Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp Tyr Val Ala Leu	
184	180 185 190	
185	Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser Pro Arg Val Lys Pro	
186	195 200 205	
187	Gln His Ile Ser Thr His Phe Leu Pro Arg Phe Lys Gln Ser Glu Gln	
188	210 215 220	
189	Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu Lys Lys Asn Pro Pro	
190	225 230 235 240	

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191 Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala Pro Arg Lys Asn Thr      DATE: 04/17/2002
192           245           250           255
193 Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe Gly
194           260           265
198 <210> SEQ ID NO: 5
199 <211> LENGTH: 531
200 <212> TYPE: DNA
201 <213> ORGANISM: Homo sapiens
203 <220> FEATURE:
204 <221> NAME/KEY: CDS
205 <222> LOCATION: (1)..(531)
207 <400> SEQUENCE: 5
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210   1           5           10          15
212 gtc aat gga tcc cac gaa gcc aat atg tta agt gtt ttg gaa ata ttt      96
213 Val Asn Gly Ser His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe
214           20           25          30
216 gct gtg tct cag ggg att gta gga ata cga gga gtt ttc agc aac aaa      144
217 Ala Val Ser Gln Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys
218           35           40          45
220 ttt tta gcg atg tca aaa aaa gga aaa ctc cat gca agt gcc aag ttc      192
221 Phe Leu Ala Met Ser Lys Lys Gly Leu His Ala Ser Ala Lys Phe
222           50           55          60
224 aca gat gac tgc aag ttc agg gag cgt ttt caa gaa aat agc tat aat      240
225 Thr Asp Asp Cys Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn
226   65           70           75          80
228 acc tat gcc tca gca ata cat aga act gaa aaa aca ggg cgg gag tgg      288
229 Thr Tyr Ala Ser Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp
230           85           90          95
232 tat gtt gcc ctg aat aaa aga gga aaa gcc aaa cga ggg tgc agc ccc      336
233 Tyr Val Ala Leu Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser Pro
234           100          105         110
236 cgg gtt aaa ccc cag cat atc tct acc cat ttt ctt cca aga ttc aag      384
237 Arg Val Lys Pro Gln His Ile Ser Thr His Phe Leu Pro Arg Phe Lys
238           115          120         125
240 caq tcg gag cag cca gaa ctt tct ttc acg gtt act gtt cct gaa aag      432
241 Gln Ser Glu Gln Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu Lys
242           130          135         140
244 aaa aat cca cct agc cct atc aag tca aag att ccc ctt tct gca cct      480
245 Lys Asn Pro Pro Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala Pro
246   145           150           155          160
248 cgg aaa aat acc aac tca gtg aaa tac aga ctc aag ttt cgc ttt gga      528
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250           165           170           175
252 taa
256 <210> SEQ ID NO: 6
257 <211> LENGTH: 176
258 <212> TYPE: PRT

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259 <213> ORGANISM: Homo sapiens
261 <100> SEQUENCE: 6
262 Cys Arg Val Gly Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys
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264 Val Asn Gly Ser His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe
265 20 25 30
266 Ala Val Ser Gln Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys
267 35 40 45
268 Phe Leu Ala Met Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe
269 50 55 60
270 Thr Asp Asp Cys Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn
271 65 70 75 80
272 Thr Tyr Ala Ser Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp
273 85 90 95
274 Tyr Val Ala Leu Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser Pro
275 100 105 110
276 Arg Val Lys Pro Gln His Ile Ser Thr His Phe Leu Pro Arg Phe Lys
277 115 120 125
278 Gln Ser Glu Gln Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu Lys
279 130 135 140
280 Lys Asn Pro Pro Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala Pro
281 145 150 155 160
282 Arg Lys Asn Thr Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe Gly
283 165 170 175
287 <210> SEQ ID NO: 7
288 <211> LENGTH: 531
289 <212> TYPE: DNA
290 <213> ORGANISM: Homo sapiens
292 <220> FEATURE:
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294 <222> LOCATION: (1)..(531)
296 <400> SEQUENCE: 7
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298 Cys Arg Val Gly Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys
299 1 5 10 15
301 gtc aat gga tcc cac gaa gcc aat atg tta agt gtt ttg gaa ata ttt 96
302 Val Asn Gly Ser His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe
303 20 25 30
305 gct gtg tct cag ggg att gta gga ata cga gga gtt ttc agc aac aaa 144
306 Ala Val Ser Gln Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys
307 35 40 45
309 ttt tta gcg atg tca aaa aaa gga aaa ctc cat gca agt gcc aag ttc 192
310 Phe Leu Ala Met Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe
311 50 55 60
313 aca gat gac tgc aag ttc agg gag cgt ttt caa gaa aat agc tat aat 240
314 Thr Asp Asp Cys Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn
315 65 70 75 80
317 acc tat gcc tca gca ata cat aga act gaa aaa aca ggg cgg gag tgg 288
318 Thr Tyr Ala Ser Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp

VERIFICATION SUMMARY
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L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M 271 C: Current Filing Date differs, Replaced Current Filing Date